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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/770,528

DATE: 11/27/2001

TIME: 11:51:37

Input Set : N:\Crf3\RULE60\09770528.txt

Output Set: N:\CRF3\11272001\I770528.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Hedrick, Joseph A.
7 Sana, Theodore R.
8 Bazan, Fernando J.
9 Kastelein, Robert A.

11 (ii) TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
12 and Methods

14 (iii) NUMBER OF SEQUENCES: 15

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: DNAX Research Institute
18 (B) STREET: 901 California
19 (C) CITY: Palo Alto
20 (D) STATE: California
21 (E) COUNTRY: USA
22 (F) ZIP: 94304-1104

ENTERED

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/770,528
C--> 32 (B) FILING DATE: 25-Jan-2001
33 (C) CLASSIFICATION:

47 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 09/130,972
37 (B) FILING DATE:
40 (A) APPLICATION NUMBER: US 60/055,111
41 (B) FILING DATE: 06-AUG-1997
44 (A) APPLICATION NUMBER: US 09/062,866
45 (B) FILING DATE: 20-APR-1998
48 (A) APPLICATION NUMBER: US 09/097,976
49 (B) FILING DATE: 16-JUN-1998

51 (viii) ATTORNEY/AGENT INFORMATION:

52 (A) NAME: Ching, Edwin P.
53 (B) REGISTRATION NUMBER: 34,090
54 (C) REFERENCE/DOCKET NUMBER: DX0725K2

56 (ix) TELECOMMUNICATION INFORMATION:

57 (A) TELEPHONE: 650-852-9196
58 (B) TELEFAX: 650-496-1200

61 (2) INFORMATION FOR SEQ ID NO: 1:

63 (i) SEQUENCE CHARACTERISTICS:

64 (A) LENGTH: 470 base pairs
65 (B) TYPE: nucleic acid
66 (C) STRANDEDNESS: single
67 (D) TOPOLOGY: linear

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69      (ii) MOLECULE TYPE: cDNA
72      (ix) FEATURE:
73          (A) NAME/KEY: CDS
74          (B) LOCATION: 1..468
77      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
79 ATG ATG GTT CTG AGT GGG GCA CTA TGC TTC CGA ATG AAG GAT TCA GCC      48
80 Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala
81 1      5      10      15
83 TTG AAG GTA CTG TAT CTG CAC AAT AAC CAG CTG CTG GCT GGA GGA CTG      96
84 Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu
85      20      25      30
87 CAC GCA GAG AAG GTC ATT AAA GGT GAG GAG ATC AGT GTT GTC CCA AAT      144
88 His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn
89      35      40      45
91 CGG GCA CTG GAT GCC AGT CTG TCC CCT GTC ATC CTG GGC GTT CAA GGA      192
92 Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly
93      50      55      60
95 GGA AGC CAG TGC CTA TCT TGT GGG ACA GAG AAA GGG CCA ATT CTG AAA      240
96 Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys
97 65      70      75      80
99 CTT GAG CCA GTG AAC ATC ATG GAG CTC TAC CTC GGG GCC AAG GAA TCA      288
100 Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser
101      85      90      95
103 AAG AGC TTC ACC TTC TAC CGG CGG GAT ATG GGT CTT ACC TCC AGC TTC      336
104 Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe
105      100      105      110
107 GAA TCC GCT GCC TAC CCA GGC TGG TTC CTC TGC ACC TCA CCG GAA GCT      384
108 Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala
109      115      120      125
111 GAC CAG CCT GTC AGG CTC ACT CAG ATC CCT GAG GAC CCC GCC TGG GAT      432
112 Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp
113      130      135      140
115 GCT CCC ATC ACA GAC TTC TAC TTT CAG CAG TGT GAC TA      470
116 Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
117 145      150      155
120 (2) INFORMATION FOR SEQ ID NO: 2:
122      (i) SEQUENCE CHARACTERISTICS:
123          (A) LENGTH: 156 amino acids
124          (B) TYPE: amino acid
125          (D) TOPOLOGY: linear
127      (ii) MOLECULE TYPE: protein
129      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
131 Met Met Val Leu Ser Gly Ala Leu Cys Phe Arg Met Lys Asp Ser Ala
132 1      5      10      15
134 Leu Lys Val Leu Tyr Leu His Asn Asn Gln Leu Leu Ala Gly Gly Leu
135      20      25      30
137 His Ala Glu Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn
138      35      40      45
140 Arg Ala Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly

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141      50      55      60
143 Gly Ser Gln Cys Leu Ser Cys Gly Thr Glu Lys Gly Pro Ile Leu Lys
144 65      70      75      80
146 Leu Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser
147      85      90      95
149 Lys Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe
150      100      105      110
152 Glu Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Ser Pro Glu Ala
153      115      120      125
155 Asp Gln Pro Val Arg Leu Thr Gln Ile Pro Glu Asp Pro Ala Trp Asp
156      130      135      140
158 Ala Pro Ile Thr Asp Phe Tyr Phe Gln Gln Cys Asp
159 145      150      155
161 (2) INFORMATION FOR SEQ ID NO: 3:
163 (i) SEQUENCE CHARACTERISTICS:
164 (A) LENGTH: 219 base pairs
165 (B) TYPE: nucleic acid
166 (C) STRANDEDNESS: single
167 (D) TOPOLOGY: linear
169 (ii) MOLECULE TYPE: cDNA
172 (ix) FEATURE:
173 (A) NAME/KEY: CDS
174 (B) LOCATION: 1..216
177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
179 TTC CAG GAA GGG AAC ATA ATG GAA ATG TAC AAC AAA AAG GAA CCT GTA      48
180 Phe Gln Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val
181 1      5      10      15
183 AAA GCC TCT CTC TTC TAT CAC AAG AAG AGT GGT ACA ACC TCT ACA TTT      96
184 Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe
185      20      25      30
187 GAG TCT GCA GCC TTC CCT GGT TGG TTC ATC GCT GTC TGC TCT AAA GGG      144
188 Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly
189      35      40      45
191 AGC TGC CCA CTC ATT CTG ACC CAA GAA CTG GGG GAA ATC TTC ATC ACT      192
192 Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr
193      50      55      60
195 GAC TTC GAG ATG ATT GTG GTA CAT TAA      219
196 Asp Phe Glu Met Ile Val Val His
197 65      70
200 (2) INFORMATION FOR SEQ ID NO: 4:
202 (i) SEQUENCE CHARACTERISTICS:
203 (A) LENGTH: 72 amino acids
204 (B) TYPE: amino acid
205 (D) TOPOLOGY: linear
207 (ii) MOLECULE TYPE: protein
209 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
211 Phe Gln Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val
212 1      5      10      15
214 Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe

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215          20          25          30
217 Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly
218          35          40          45
220 Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr
221          50          55          60
223 Asp Phe Glu Met Ile Val Val His
224 65          70
226 (2) INFORMATION FOR SEQ ID NO: 5:
228 (i) SEQUENCE CHARACTERISTICS:
229 (A) LENGTH: 809 base pairs
230 (B) TYPE: nucleic acid
231 (C) STRANDEDNESS: single
232 (D) TOPOLOGY: linear
234 (ii) MOLECULE TYPE: cDNA
237 (ix) FEATURE:
238 (A) NAME/KEY: CDS
239 (B) LOCATION: 90..569
242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
244 GAATTCGGCA CGAGTGTAGT GTGCAGACAC ATTCCTTATT CAATCAGGGT CAATCTGCAG 60
246 ATGGGCAGCT CAGGAACAAC ATCACCATA ATG AAT AAG GAG AAA GAA CTA AGA 113
247 Met Asn Lys Glu Lys Glu Leu Arg
248 1 5
250 GCA GCA TCA CCT TCG CTT AGA CAT GTT CAG GAT CTT AGT AGT CGT GTG 161
251 Ala Ala Ser Pro Ser Leu Arg His Val Gln Asp Leu Ser Ser Arg Val
252 10 15 20
254 TGG ATC CTG CAG AAC AAT ATC CTC ACT GCA GTC CCA AGG AAA GAG CAA 209
255 Trp Ile Leu Gln Asn Asn Ile Leu Thr Ala Val Pro Arg Lys Glu Gln
256 25 30 35 40
258 ACA GTT CCA GTC ACT ATT ACC TTG CTC CCA TGC CAA TAT CTG GAC ACT 257
259 Thr Val Pro Val Thr Ile Thr Leu Leu Pro Cys Gln Tyr Leu Asp Thr
260 45 50 55
262 CTT GAG ACG AAC AGG GGG GAT CCC ACG TAC ATG GGA GTG CAA AGG CCG 305
263 Leu Glu Thr Asn Arg Gly Asp Pro Thr Tyr Met Gly Val Gln Arg Pro
264 60 65 70
266 ATG AGC TGC CTG TTC TGC ACA AAG GAT GGG GAG CAG CCT GTG CTA CAG 353
267 Met Ser Cys Leu Phe Cys Thr Lys Asp Gly Glu Gln Pro Val Leu Gln
268 75 80 85
270 CTT GGG GAA GGG AAC ATA ATG GAA ATG TAC AAC AAA AAG GAA CCT GTA 401
271 Leu Gly Glu Gly Asn Ile Met Glu Met Tyr Asn Lys Lys Glu Pro Val
272 90 95 100
274 AAA GCC TCT CTC TTC TAT CAC AAG AAG AGT GGT ACA ACC TCT ACA TTT 449
275 Lys Ala Ser Leu Phe Tyr His Lys Lys Ser Gly Thr Thr Ser Thr Phe
276 105 110 115 120
278 GAG TCT GCA GCC TTC CCT GGT TGG TTC ATC GCT GTC TGC TCT AAA GGG 497
279 Glu Ser Ala Ala Phe Pro Gly Trp Phe Ile Ala Val Cys Ser Lys Gly
280 125 130 135
282 AGC TGC CCA CTC ATT CTG ACC CAA GAA CTG GGG GAA ATC TTC ATC ACT 545
283 Ser Cys Pro Leu Ile Leu Thr Gln Glu Leu Gly Glu Ile Phe Ile Thr
284 140 145 150

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286 GAC TTC GAG ATG ATT GTG GTA CAT TAAGGTTTTT AGACACATTG CTCTGTGGCA      599
287 Asp Phe Glu Met Ile Val Val His
288      155      160
290 CTCTCTCAAG ATTTCTTGGA TTCTAACAAG AAGCAATCAA AGACACCCCT AACAAAATGG      659
292 AAGACTGAAA AGAAAGCTGA GCCCTCCCTG GGCTGTTTTT CCTTGGTGGT GAATCAGATG      719
294 CAGAACATCT TACCATGTTT TCATCCAAAG CATTACTGT TGTTTTTAC AAGGAGTGAA      779
296 TTTTTTAAAA TAAAATCATT TATCTCATAA      809
299 (2) INFORMATION FOR SEQ ID NO: 6:
301 (i) SEQUENCE CHARACTERISTICS:
302 (A) LENGTH: 160 amino acids
303 (B) TYPE: amino acid
304 (D) TOPOLOGY: linear
306 (ii) MOLECULE TYPE: protein
308 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
310 Met Asn Lys Glu Lys Glu Leu Arg Ala Ala Ser Pro Ser Leu Arg His
311 1      5      10      15
313 Val Gln Asp Leu Ser Ser Arg Val Trp Ile Leu Gln Asn Asn Ile Leu
314      20      25      30
316 Thr Ala Val Pro Arg Lys Glu Gln Thr Val Pro Val Thr Ile Thr Leu
317      35      40      45
319 Leu Pro Cys Gln Tyr Leu Asp Thr Leu Glu Thr Asn Arg Gly Asp Pro
320      50      55      60
322 Thr Tyr Met Gly Val Gln Arg Pro Met Ser Cys Leu Phe Cys Thr Lys
323 65      70      75      80
325 Asp Gly Glu Gln Pro Val Leu Gln Leu Gly Glu Gly Asn Ile Met Glu
326      85      90      95
328 Met Tyr Asn Lys Lys Glu Pro Val Lys Ala Ser Leu Phe Tyr His Lys
329      100      105      110
331 Lys Ser Gly Thr Thr Ser Thr Phe Glu Ser Ala Ala Phe Pro Gly Trp
332      115      120      125
334 Phe Ile Ala Val Cys Ser Lys Gly Ser Cys Pro Leu Ile Leu Thr Gln
335      130      135      140
337 Glu Leu Gly Glu Ile Phe Ile Thr Asp Phe Glu Met Ile Val Val His
338 145      150      155      160
341 (2) INFORMATION FOR SEQ ID NO: 7:
343 (i) SEQUENCE CHARACTERISTICS:
344 (A) LENGTH: 177 amino acids
345 (B) TYPE: amino acid
346 (C) STRANDEDNESS: not relevant
347 (D) TOPOLOGY: linear
349 (ii) MOLECULE TYPE: peptide
354 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
356 Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu
357 1      5      10      15
359 Phe Leu Phe His Ser Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser
360      20      25      30
362 Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe
363      35      40      45
365 Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn

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VERIFICATION SUMMARY

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]